

OM protein - protein search, using sw model

Run on: November 3, 2005, 08:19:03 ; Search time 181 Seconds
(without alignments)
1496.629 Million cell updates/sec

Title: US-10-628-432-32

Sequence: 1 MSQTGSHPRGLAGRLMGA.....DQLDFNIPQAVDYKDDDDK 529

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2805	98.1	837	1 AT54_HUMAN	O75173 homo sapien
2	2798	97.9	837	2 O6UMA8	O6UMA8 homo sapien
3	2790	97.6	837	2 O6P408	O6P408 homo sapien
4	2557	89.4	839	2 O7YS95	O7YS95 bos taurus
5	2460	86.0	845	2 O8BNJ2	O8BNJ2 mus musculu
6	2459	86.0	833	2 O8K384	O8K384 mus musculu
7	2248	78.6	893	2 O6A017	O6A017 mus musculu
8	1659	58.0	339	2 O8NEX2	O8NEX2 mus musculu
9	1613	56.4	630	1 AT54_RAT	O9E8P7 mus musculu
10	1222	42.7	968	1 AT51_RAT	O9E8P7 mus musculu
11	1221.5	42.7	967	1 AT51_MOUSE	O9E8P7 mus musculu
12	1220.5	42.7	967	2 O6BEJ2	O9E8P7 mus musculu
13	1193	41.7	967	1 AT51_HUMAN	O9E8P7 mus musculu
14	1193	41.7	967	2 O8NEX2	O9E8P7 mus musculu
15	1108	38.8	245	1 AT54_BOVIN	O9E8P7 mus musculu
16	1095	38.3	950	1 AT54_HUMAN	O9E8P7 mus musculu
17	1084	37.9	203	2 O8NEX2	O9E8P7 mus musculu
18	1061	37.1	192	2 O8NEX2	O9E8P7 mus musculu
19	1053.5	36.8	890	1 AT54_HUMAN	O9E8P7 mus musculu
20	1049.5	36.7	759	2 O8NEX2	O9E8P7 mus musculu
21	1011.5	35.4	905	1 AT58_MOUSE	O9E8P7 mus musculu
22	858	30.0	1906	1 AT20_MOUSE	O9E8P7 mus musculu
23	847	29.6	867	2 O6FKM3	O9E8P7 mus musculu
24	837.5	29.3	928	2 AT55_MOUSE	O9E8P7 mus musculu
25	830.5	29.0	928	2 O6TY19	O9E8P7 mus musculu
26	827	28.9	930	1 AT58_HUMAN	O9E8P7 mus musculu
27	822	28.8	1935	1 AT58_HUMAN	O9E8P7 mus musculu
28	786	27.5	1911	1 AT20_HUMAN	O9E8P7 mus musculu
29	706.5	24.7	2165	1 Q19791	O9E8P7 mus musculu
30	650.5	22.8	997	1 Q19791	O9E8P7 mus musculu
31	649.5	22.7	1686	2 O6P7J9	O9E8P7 mus musculu

32	646	22.6	623	2 O8BGP4	O8BGP4 m. mus. muscu
33	642	22.5	1641	2 O6BSA9	O6BSA9 mus musculu
34	637	22.3	1593	.1 AT12_HUMAN	P58397 homo sapien
35	635	22.2	117	2 O8VHK4	O8VHK4 mus musculu
36	608	21.3	1009	2 O8BKX1	O8BKX1 m. mus. muscu
37	608	21.3	1600	2 O8B1B3	O8B1B3 mus musculu
38	598.5	20.9	1095	1 AT17_HUMAN	O8E565 homo sapien
39	570	19.9	1077	1 AT10_HUMAN	O8E565 homo sapien
40	565.5	19.8	988	2 O7PWT7	O7PWT7 anophelid g
41	564	19.7	1070	2 O8CG28	O8CG28 mus musculu
42	561.5	19.6	769	2 O8MR15	O8MR15 drosophila
43	560.5	19.6	1221	2 O6P4R5	O6P4R5 homo sapien
44	555.5	19.4	1059	2 O9W493	O9W493 drosophila
45	550	19.2	1081	1 AT18_HUMAN	O8E660 homo sapien

ALIGNMENTS

RESULT 1
AT54_HUMAN
ID 075173, OSUN83, STANDARD; PRT; 837 AA.
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE ADAMTS-4 precursor (EC 3.4.24.82) (A disintegrin and metalloproteinase
DE with thrombospondin motifs 4) (ADAM-TS 4) (ADAM-TS4) (Aggrecanase 1)
DE (ADMP-1).
GN Name=ADAMTS4; Synonyms=K1RA0688;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
RA Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99286303; PubMed=10356395; DOI=10.1126/science.284.5420.1664;
RA Tortorella M.D., Burn T.C., Pratta M.A., Abbazade I., Hollis J.M.,
RA Liu R.-Q., Rosenfeld S.A., Copeland R.A., Decicco C.P., Wynn R.,
RA Rockwell A., Yang F., Duke J.L., Solomon K., George H., Bruckner R.,
RA Nagase H., Itoh Y., Ellis D.M., Ross H., Wiswall B.H., Murphy K.,
RA Hillman M.C. Jr., Hollis G.F., Newton R.C., Magolda R.L.,
RA Tzabatos J.M., Arner E.C.;
RT "Purification and cloning of aggrecanase-1: a member of the ADAMTS
RT family of proteases.";
RN [3]
RP Science 284:1664-1666(1999).
RA Sawai Y., Nagase H., Saklatvala J., Clark A.R.;
RT "ADAMTS-4 genomic locus.";
RN [4]
RP Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
PARTIAL SEQUENCE, AND CHARACTERIZATION.
RX MEDLINE=20400518; PubMed=10827174; DOI=10.1074/jbc.M001065200;
RA Tortorella M.D., Pratta M.A., Liu R.-Q., Abbazade I., Rose H.,
RA Burn T.C., Arner E.C.;
RT "The thrombospondin motif of aggrecanase-1 (ADAMTS-4) is critical for
RT aggrecan substrate recognition and cleavage.";
RN [5]
RX J. Biol. Chem. 275:25791-25797(2000).
CC -1- FUNCTION: Cleaves aggrecan, a cartilage proteoglycan, and may be
CC involved in its turnover. May play an important role in the
CC destruction of aggrecan in arthritic diseases. Could also be a
CC critical factor in the exacerbation of neurodegeneration in

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OM protein - protein search, using sw model

Run on: November 3, 2005, 08:19:43 ; Search time 41 Seconds

(without alignments)
1241.431 Million cell updates/sec

Title: US-10-628-432-32

Perfect score: 2859

Sequence: 1 MSQTSHPGRGLAGRWLMGA.....DQLDFNIPQAVYKDDDDK 529

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2801	98.0	837	2 T00355	hypothetical prote
2	1222	42.7	951	2 T00017	gene ADAMTS-1 prot
3	706.5	24.7	2165	2 T1371	hypothetical prote
4	479.5	16.8	1205	2 T1817	procollagen N-endo
5	436.5	15.3	550	2 T47158	hypothetical prote
6	277.5	9.7	860	2 T16892	hypothetical prote
7	277.5	9.7	1444	2 T18856	angiogenesis inhib
8	268.5	9.4	903	2 S60257	meltrin alpha - mo
9	250	8.7	480	1 A30065	triglycan precuro
10	236.5	8.3	407	2 S66260	metalloproteinase
11	234	8.2	609	2 S55270	cactocollastatin p
12	231.5	8.1	814	2 G03390	disintegrin-like m
13	230	8.0	478	2 A43296	hemorrhagic protei
14	227.5	8.0	478	2 J01301	ecarin precursor
15	225.5	7.9	571	2 S24789	fibriolytic metal
16	224	7.8	616	2 A55796	metalloproteinase
17	221.5	7.7	478	2 J04880	acrtolysin A (EC 3
18	221	7.7	481	2 J04342	acrtolysin C (EC 3
19	218.5	7.6	549	2 S48169	metalloproteinase
20	217.5	7.6	419	2 S41607	acrtolysin A (EC 3
21	217	7.6	481	2 S43125	acrtolysin C (EC 3
22	214.5	7.5	617	1 HYSRAC	metalloproteinase
23	214	7.5	617	1 HYSRAC	metalloproteinase
24	211.5	7.4	411	1 HYSNRA	acrtolysin C (EC 3
25	210.5	7.4	411	1 HYSNRA	acrtolysin C (EC 3
26	210	7.3	508	2 T22836	hypothetical prote
27	207.5	7.3	826	2 A60365	monocyte surface a
28	200	7.0	484	2 J08020	metalloproteinase
29	199.5	7.0	610	2 J07530	vacuolar apoptosis

30	193.5	6.8	414	2 S41608	acrtolysin B (EC 3
31	192.5	6.7	610	2 J08056	halysae - Glycidu
32	192.5	6.7	655	2 J07850	disintegrin and me
33	185.5	6.5	429	2 A42972	coagulation factor
34	183.5	6.4	952	2 T18900	disintegrin and me
35	174.5	6.1	957	2 T18900	hypothetical prote
36	172	6.0	670	2 T18900	disintegrin-like m
37	171	6.0	789	2 S28259	androgen-regulated
38	170.5	6.0	419	2 A59414	metalloproteinase
39	167	5.8	524	2 S38539	disintegrin-like m
40	167	5.8	660	2 S71949	metalloproteinase
41	164.5	5.8	905	2 S55059	disintegrin-like m
42	164	5.7	200	2 S1511	metalloproteinase
43	164	5.7	203	2 A59421	fertilin alpha-1 -
44	163	5.7	825	2 A55060	hemorrhagic factor
45	156	5.5	416	2 A37877	metalloproteinase
					fertilin alpha-11
					hemorrhagic protei

ALIGNMENTS

RESULT 1

T00355
hypothetical protein KIAA0688 - human
C/Species: Homo sapiens (man)
C/Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C/Accession: T00355
R/Chikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.
DNA Res. 5, 169-176, 1998
A/Title: Prediction of the coding sequences of unidentified human genes. X. The complet
A/Reference number: Z14142; MUID:98403880; PMID:9734811
A/Accession: T00355
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-837 <1SH>
A/Cross-references: UNIPROT:075173; EMBL:AB014588; NID:93327189; PIDN:BAA1663.1; PID:G
A/Experimental source: brain
C/Genetics:
A/Genes: KIAA0688
F:519-575/Domain: thrombospondin type 1 repeat homology <THR3>

Query Match 98.0%; Score 2801; DB 2; Length 837;
Best Local Similarity 99.6%; Pred. No. 3 9e-200;
Matches 518; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	MSQTSHPGRGLAGRWLMGAQPCLLPVLSWLVLLLLASLPRLAPLPRER	60
DB	1	MSQTSHPGRGLAGRWLMGAQPCLLPVLSWLVLLLLASLPRLAPLPRER	60
QY	61	IVFEKLVGSLVPGSGAPARLLCRLOAGETLLLEEDSGVQVEGLTVQYLGQAFELG	120
DB	61	IVFEKLVGSLVPGSGAPARLLCRLOAGETLLLEEDSGVQVEGLTVQYLGQAFELG	120
QY	121	GAEPQTVLTGTINGDPESVASLHMDGALLGVLOVRGAELHQLPLEGTPNSAGPGAH	180
DB	121	GABPQTVLTGTINGDPESVASLHMDGALLGVLOVRGAELHQLPLEGTPNSAGPGAH	180
QY	181	LRRSPASGQPMCNVAPLPGSPRRPRARAFSLSFVETLVVADDKMAAFHAGLKR	240
DB	181	LRRSPASGQPMCNVAPLPGSPRRPRARAFSLSFVETLVVADDKMAAFHAGLKR	240
QY	241	YLLVMAAAAFHGRPIRNPVSLVTRLVLTGSGEERGPGVPSAAQTLRFSCAQRGILN	300
DB	241	YLLVMAAAAFHGRPIRNPVSLVTRLVLTGSGEERGPGVPSAAQTLRFSCAQRGILN	300
QY	301	TPEDSDPDHEDTALLFRQDLGVSCTDTGMAVGTVCQPARSCATVEDDGLSAPFA	360
DB	301	TPEDSDPDHEDTALLFRQDLGVSCTDTGMAVGTVCQPARSCATVEDDGLSAPFA	360
QY	361	HQGHVNTMLHNSKPCISLNGPLSTRHVAAPYMAVDEEPPSPCSARFITFDLNGY	420
DB	361	HELGHVNTMLHNSKPCISLNGPLSTRHVAAPYMAVDEEPPSPCSARFITFDLNGY	420

Run on: November 3, 2005, 08:15:58 ; Search time 165 Seconds

(without alignments)
1239.977 Million cell updates/sec

US-10-628-432-32

Perfect score: 2859
Sequence: 1 MSQTGSHPGRLAGRLWGA.....DQLDFNIPQAVDYKDDDDK 529

scoring table: BLOSUM62

gaprop 10.0 , Gapext 0.5

2105692 seqs, 386760381 residues

total number of rules satisfying chosen parameters: 2105692

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

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1:  geneseqp1980s:*
2:  geneseqp1990s:*
3:  geneseqp2000s:*
4:  geneseqp2001s:*
5:  geneseqp2002s:*
6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2859	100.0	529	8	ADS20235	Ads20235 Human agc
2	2821.5	98.7	584	8	ADS20234	Ads20234 Human agc
3	2808	98.2	846	8	ADS20232	Ads20232 Human agc
4	2805	98.1	686	8	ADS20229	Ads20229 Human agc
5	2805	98.1	697	8	ADS20227	Ads20227 Human agc
6	2805	98.1	837	2	AAW75425	Aaw75425 Human agc
7	2805	98.1	837	2	ADJ65945	Adj65945 Human agc
8	2805	98.1	837	7	ADS20209	Ads20209 Human agc
9	2804	98.1	845	8	ADS20202	Ads20202 Human agc
10	2801	98.0	520	7	ADBS85490	Adbs85490 Human agc
11	2801	98.0	575	7	ADBS85489	Adbs85489 Human agc
12	2801	98.0	837	7	AAAG78228	Aag78228 Human agc
13	2801	98.0	837	7	ADBS85488	Adbs85488 Human agc
14	2801	98.0	840	3	AAAB61178	Aaab61178 Human agc
15	2798	98.0	840	3	AAAB61178	Aaab61178 Human agc
16	2798	97.9	837	3	AAAB61178	Aaab61178 Human agc
17	2798	97.9	837	4	AAAB61178	Aaab61178 Human agc
18	2798	97.9	837	6	ABUS8575	Abus8575 Human agc
19	2798	97.9	837	6	ABUS8575	Abus8575 Human agc
20	2798	97.9	837	6	ABUS8575	Abus8575 Human agc
21	2798	97.9	837	6	ABUS8575	Abus8575 Human agc
22	2798	97.9	837	6	ABUS8575	Abus8575 Human agc
23	2798	97.9	837	6	ABUS8575	Abus8575 Human agc
24	2798	97.9	837	6	ABUS8575	Abus8575 Human agc
25	2798	97.9	837	6	ABUS8575	Abus8575 Human agc

26	2798	97.9	837	6	ABR68251	Human	sec
27	2798	97.9	837	6	ABU96304	Novel	hunn
28	2798	97.9	837	6	ABU92735	Human	sec
29	2798	97.9	837	6	ABO08812	Human	sec
30	2798	97.9	837	6	ABO02864	Human	sec
31	2798	97.9	837	6	ABR75018	Human	sec
32	2798	97.9	837	6	ABR94780	Human	sec
33	2798	97.9	837	6	ABU85753	Human	sec
34	2798	97.9	837	6	ABU98913	Human	PRC
35	2798	97.9	837	6	ABU98128	Novel	hunn
36	2798	97.9	837	6	ABU91834	Novel	hunn
37	2798	97.9	837	6	ABU89527	Human	PRC
38	2798	97.9	837	6	ABU85368	Human	sec
39	2798	97.9	837	6	ABU87581	Human	sec
40	2798	97.9	837	6	ABU80609	Human	PRC
41	2798	97.9	837	6	ABR93527	Human	sec
42	2798	97.9	837	6	ABR98917	Human	sec
43	2798	97.9	837	6	ABO16440	Human	sec
44	2798	97.9	837	6	ABR92340	Human	sec
45	2798	97.9	837	6	ABO18981	Human	sec

ALIGNMENTS

RESULT 1
ADS20235

ID	Standard; protein; 529 AA
XX	

AC ADS20235
YY

DT 18-NOV-2004 (first entry)
XX

XX **aggrecanase ADAM154 truncated/mutant E362Q protein with FLAG tag 2**

chromospondin type I motif A; metalloproteinase;
ADAM15; a disintegrin-like and metalloprotease;

aggreganase; osteopathic; antinflammatory; antiarthritic; antirheumatic, cytostatic; osteoarthritis; glioma; cancer; inflammation; joint

human; enzyme; chromosome 1q21-q23; trypsinogen; ELAC; Crohn's disease; biliary cirrhosis; septic arthritis; periodontal; KW

OS Homo sapiens.

Synthetic.

FH	Key	Location/Qualifiers
BT	Misc-414600000000000000	100

FT	note="Wild-type Glu substituted by Gln"
Misc-difference	521 529

/note= "Wild-type residues 521-837 replaced by FLAG tag"

PN WO2004011637-A2

05-FEB-2004 PD
yy

29-JUL-2003; 2003WO-US023484

23-JUL-2002; 200205-0398721P

CORCORAN C. J. (CORC/)

PA (ZENG/) ZENG W.

PA
(MCDONAGH T. MCDONAGH T.

(GEOR/) GEORGADIS K E.

2000

Freeman BA, Georgiadis KE, Lavallie ER;

WPI; 2004-143860/14

OM protein - protein search, using SW model

Run on: November 3, 2005, 08:20:33 (Search time 42 Seconds
(without alignment))
940.223 Million cell updates/sec

Title: US-10-628-432-32
Perfect score: 2859
Sequence: 1 MSQTSHPGRGLAGRLMGA.....DQIDPNIPOAVDYKDDDK 529

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2805	98.1	837	4	US-09-122-126B-2 Sequence 2, Appli
2	2805	98.1	837	4	US-09-634-286A-2 Sequence 2, Appli
3	2805	98.1	837	4	US-10-247-685-2 Sequence 2, Appli
4	1222	42.7	950	4	US-09-321-987B-4 Sequence 4, Appli
5	1193	41.7	967	4	US-09-130-491-2 Sequence 2, Appli
6	1189	41.6	949	4	US-09-568-559-2 Sequence 1, Appli
7	1097	38.4	950	4	US-10-009-332-1 Sequence 12, Appli
8	1050	36.7	727	4	US-09-445-023A-12 Sequence 9, Appli
9	1046.5	36.6	727	4	US-09-369-364A-9 Sequence 15, Appli
10	1011.5	35.4	905	4	US-09-130-491-13 Sequence 13, Appli
11	852.5	29.8	608	4	US-09-369-364A-15 Sequence 15, Appli
12	837.5	29.3	930	4	US-09-122-126B-15 Sequence 15, Appli
13	827	28.9	930	4	US-09-634-286A-15 Sequence 15, Appli
14	827	28.9	930	4	US-09-369-364A-15 Sequence 15, Appli
15	827	28.9	930	4	US-09-369-364A-15 Sequence 15, Appli
16	783.5	27.4	1882	3	US-09-369-364A-13 Sequence 13, Appli
17	733	25.6	874	3	US-09-321-987B-2 Sequence 11, Appli
18	717	25.1	2150	4	US-09-800-729-155 Sequence 15, Appli
19	706.5	24.7	2165	4	US-09-369-364A-11 Sequence 11, Appli
20	645.5	22.6	245	3	US-09-369-364A-7 Sequence 7, Appli
21	636	22.2	245	3	US-09-369-364A-11 Sequence 11, Appli
22	592	20.7	589	4	US-09-663-791-12 Sequence 12, Appli
23	592	20.7	589	4	US-09-663-791-12 Sequence 12, Appli
24	574	20.1	1104	4	US-09-881-953A-4 Sequence 4, Appli
25	559.5	19.6	438	4	US-09-663-791-22 Sequence 22, Appli
26	559.5	19.6	438	4	US-09-663-791-22 Sequence 22, Appli
27	544.5	19.0	507	4	US-09-963-791-10 Sequence 10, Appli

28	512	17.9	356	4	US-09-963-791-20 Sequence 20, Appli
29	505.5	17.7	1224	4	US-09-930-872-4 Sequence 4, Appli
30	505.5	17.7	1224	4	US-10-217-774-4 Sequence 4, Appli
31	485.5	17.0	1211	4	US-09-949-016-11401 Sequence 11, Appli
32	479.5	16.8	969	4	US-09-321-987B-5 Sequence 5, Appli
33	479.5	16.8	1211	4	US-09-491-522-5 Sequence 5, Appli
34	468.5	16.4	566	4	US-09-949-016-7010 Sequence 7, Appli
35	468.5	16.4	566	4	US-09-949-016-8505 Sequence 7, Appli
36	467	16.3	566	4	US-09-481-522-7 Sequence 7, Appli
37	451	15.8	468	4	US-09-963-791-6 Sequence 6, Appli
38	449	15.7	1081	3	US-09-369-364A-17 Sequence 17, Appli
39	448.5	15.7	1205	4	US-09-491-522-11 Sequence 11, Appli
40	435.5	15.2	551	4	US-09-130-491-16 Sequence 16, Appli
41	426	14.9	859	3	US-09-369-364A-5 Sequence 5, Appli
42	424.5	14.8	353	4	US-09-270-767-12624 Sequence 16, Appli
43	418.5	14.6	317	4	US-09-963-791-16 Sequence 16, Appli
44	403.5	14.1	1039	4	US-09-949-016-7859 Sequence 2, Appli
45	358	12.5	491	4	US-09-930-872-2

ALIGNMENTS

RESULT 1
US-09-122-126B-2
Sequence 2, Appli Application US/09122126B
Patent No. 6451575
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
FILE REFERENCE: DM6909
CURRENT APPLICATION NUMBER: US/09/122,126B
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 837
TYPE: PRT
ORGANISM: Homo sapiens
US-09-122-126B-2

Query Match	98.1%	Score 2805;	DB 4;	Length 837;
Best Local Similarity	99.8%	Pred. No. 2,1e-245;		
Matches 519;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
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QY	61	IVPEKINGSVLPSSGAPARLLCRLQAFGRTLLLEBDSGVQVEGLTVQYLGAPBELLG	120	
DB	61	IVPEKINGSVLPSSGAPARLLCRLQAFGRTLLLEBDSGVQVEGLTVQYLGAPBELLG	120	
QY	121	GAERGTYLGTINGDPESVASLHWDGALLGVLYRGAEHLQPLEGGTPNSAGRGNI	180	
DB	121	GAERGTYLGTINGDPESVASLHWDGALLGVLYRGAEHLQPLEGGTPNSAGRGNI	180	
QY	181	LRKSPASGCGPMCNVAPLGSPPRRRAKRFASLSRPVETLVVADKMAAFGAGLKR	240	
DB	181	LRKSPASGCGPMCNVAPLGSPPRRRAKRFASLSRPVETLVVADKMAAFGAGLKR	240	
QY	241	YLLTVAALAAKAPKHSIRNPVSLVYTRVYLLSGSGEGPOVGSAAOTLRSFCAMQGLN	300	
DB	241	YLLTVAALAAKAPKHSIRNPVSLVYTRVYLLSGSGEGPOVGSAAOTLRSFCAMQGLN	300	
QY	301	TPEDSDPDHFDTAILETRQDLGVSTCDPTLGMADVGVCPARSCAIVEDGLOSAFTAA	360	
DB	301	TPEDSDPDHFDTAILETRQDLGVSTCDPTLGMADVGVCPARSCAIVEDGLOSAFTAA	360	
QY	361	HOLGHVFNMLHNSKRCISLNGPLSTSRHVMAVPMVAHVDPBEPWSPCSARFITDFLDNGY	420	
DB	361	HOLGHVFNMLHNSKRCISLNGPLSTSRHVMAVPMVAHVDPBEPWSPCSARFITDFLDNGY	420	

OM protein - protein search, using sw model

Run on: November 3, 2005, 08:23:29 ; Search time 170 Seconds
(without alignments)
1301.992 Million cell updates/sec

Title: US-10-628-432-32

Perfect score: 2859

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
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22: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2859	100.0	529	16 US-10-628-432-32	Sequence 32, Appl
2	2821.5	98.7	584	16 US-10-628-432-31	Sequence 31, Appl
3	2805	98.2	846	16 US-10-628-432-29	Sequence 29, Appl
4	2805	98.1	697	16 US-10-628-432-26	Sequence 26, Appl
5	2805	98.1	697	16 US-10-628-432-24	Sequence 24, Appl
6	2805	98.1	837	14 US-10-247-685-2	Sequence 2, Appl
7	2805	98.1	837	16 US-10-408-765A-1148	Sequence 1348, Ap
8	2805	98.1	847	16 US-10-628-432-1	Sequence 1, Appl
9	2804	98.0	845	16 US-10-628-432-40	Sequence 40, Appl
10	2801	98.0	520	15 US-10-358-283-13	Sequence 13, Appl
11	2801	98.0	575	15 US-10-358-283-12	Sequence 12, Appl

12	2801	98.0	837	15 US-10-358-283-11	Sequence 11, Appl
13	2798	97.9	837	10 US-09-946-374-317	Sequence 317, App
14	2798	97.9	837	13 US-10-052-586-352	Sequence 352, App
15	2798	97.9	837	14 US-10-174-590-352	Sequence 352, App
16	2798	97.9	837	14 US-10-176-758-352	Sequence 352, App
17	2798	97.9	837	14 US-10-175-737-352	Sequence 352, App
18	2798	97.9	837	14 US-10-174-581-352	Sequence 352, App
19	2798	97.9	837	14 US-10-176-483-352	Sequence 352, App
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44	2798	97.9	837	14 US-10-176-985-352	Sequence 352, App
45	2798	97.9	837	14 US-10-176-987-352	Sequence 352, App

ALIGNMENTS

RESULT 1
US-10-628-432-32
Sequence 32, Application US/10628432
Publication No. US20040142863A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: AM101378
CURRENT APPLICATION NUMBER: US/10/628-432
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.1
SEQ ID NO 32
LENGTH: 529
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Truncated ADAMTS4 ASM
US-10-628-432-32

Query Match 100.0%, Score 2859, DB 16, Length 529;
Best Local Similarity 100.0%, Pred. No. 3.5e-231;
Matches 529, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

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Qy	121	GAPGTYLTCTINGDESVASLIMDGALLGVLOYGAEHLIPLLEGTPNSAGPGANH	180
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